AUSTRALIA

PATENTS ACT 1990

641081

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PATENT REQUEST : STANDARD PATENT

I/We being the person(s) identified below as the Applicant(s), request the grant of a patent to the person(s) identified below as the Nominated Person(s), for an invention described in the accompanying standard complete specification.

Full application details follow:

[71/70] Applicant(s)/Nominated Person(s):

Boehringer Mannheim GmbH

of

Sandhofer Strasse 112-132, D-6800 Mannheim-Waldhof, Germany

[54] Invention Title:

Improved activation of recombinant proteins

[72] Name(s) of actual inventor(s):

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Basic Convention Application(s) Details:

[31] Application Number	[33] Country	Code	[32] Date of Application
P 41 05 480.6	Germany	DE	21 February 1991

DATED this FOURTEENTH day of FEBRUARY 1992

.....

a member of the firm of
DAVIES COLLISON CAVE for
and on behalf of the
applicant(s)

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NOTICE OF ENTITLEMENT

We, **Boehringer Mannheim GmbH**, the applicant/Nominated Person named in the accompanying Patent Request state the following:-

The Nominated Person is entitled to the grant of the patent because the Nominated Person would, on the grant of a patent for the invention to the inventors, be entitled to have the patent assigned to the Nominated Person.

The Nominated Person is entitled to claim priority from the basic application listed on the patent request because the Nominated Person made the basic application, and because that application was the first application made in a Convention country in respect of the invention.

DATED this FOURTEENTH day of FEBRUARY 1992

a member of the firm of
DAVIES COLLISON
CAVE for and on behalf
of the applicant(s)

(DCC ref: 1477617)

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(12) PATENT ABRIDGMENT (11) Document No. AU-B-10948/92
(19) AUSTRALIAN PATENT OFFICE (10) Acceptance No. 641081

(54) Title
IMPROVED ACTIVATION OF RECOMBINANT PROTEINS

International Patent Classification(s)
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(57,

The achievement of the object according to the present invention is based on the surprising observation that the renaturation yield of a protein is increased when additional helper sequences are added to its N- or/and C-terminus.

CLAIM

1. Process for the activation of recombinant proteins which are present in at least a partially inactive form, wherein a protein is activated by known solubilisation or/and renaturation techniques, said protein having additional helper sequences 2 to 50 amino acids in length at its N- or/and C-terminus added to said recombinant protein by adding oligonucleotide sequence encoding said helper sequence to at least one end of a DNA sequence encoding said recombinant protein and whereby the relative hydrophobicity of these helper sequences, which is calculated as the sum of the relative hydrophobicities specified in Table 1 for the individual amino acids, has a negative numerical value.

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AUSTRALIA

PATENTS ACT 1950

COMPLETE SPECIFICATION

NAME OF APPLICANT(S):

Boehringer Mannheim GmbH

ADDRESS FOR SERVICE:

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Patent Attorneys
1 Little Collins Street, Melbourne, 3000.

INVENTION TITLE:

Improved activation of recombinant proteins

The following statement is a full description of this invention, including the best method of performing it known to me/us:-

Description

The present invention concerns a process for the activation of recombinant proteins, in particular for the activation of recombinant proteins from prokaryotes.

When recombinant proteins are expressed in prokaryotes the proteins are often produced in the host cell in the form of at least partially inactive, sparingly soluble aggregates (refractile bodies, inclusion bodies IB) which furthermore may also be contaminated with proteins of the host cell. Before such proteins can be used, for example for therapeutic or diagnostic purposes, they must be converted into their active form.

Processes for the renaturation of recombinant proteins are generally known and disclosed for example in EP-A 0 114 506, WO 86/00610, WO 84/03711, US 4,530,787 and in EP-A 0 241 022. However, when activating natural protein sequences low yields are often obtained with these known methods. The underlying object of the present invention is therefore to achieve an improvement in the renaturation yields of recombinant proteins. In principle it would have been possible to achieve this by providing a process in which the yields are improved by selection of renaturation conditions. This is, however, not the subject matter of the present invention.

The achievement of the object according to the present invention is based on the surprising observation that the renaturation yield of a protein is increased when additional helper sequences are added to its N- or/and C-terminus.

The present invention therefore provides a process for the activation of recombinant proteins, in particular of recombinant proteins from prokaryotes which are present in at least a partially inactive form, whereby this process is characterized in that a protein is activated by known solubilization or/and renaturation techniques, said protein having additional helper sequences 2 to 50 amino acids in length at its N- or/and C-terminus whereby the relative hydrophobicities of these helper sequences, which are calculated as the sum of the relative hydrophobicities specified in Table 1 for the individual amino acids, has a negative numerical value.

The term "relative hydrophobicity" as used within the sense of the present invention is derived from the citations T.E. Creighton (1983), Proteins, Structure and Molecular Principles, W.H. Freeman and Company, New York, p. 142, Table 4.4; G. von Heijne and C. Blomberg (1979) Eur.J.Biochem. 95, 175-181 and Y. Nozaki and C. Tanford (1971), J.Biol.Chem. 246, 2211-2217. The value for the relative hydrophobicity of an amino acid is determined e.g. according to Nozaki/Tanford by determination of the partition equilibrium of this amino acid between a non-polar solvent (e.g. ethanol/dioxan) and water. The relative hydrophobicity is an energy quantity and is thus stated in kcal/mol. A positive value for the relative hydrophobicity means that there is a preference for non-polar solvents, i.e. that it is a non-polar amino acid. If in contrast the relative hydrophobicity has a numerical value which is smaller than 0 then it is a polar amino acid which has a preference for water compared to a non-polar solvent. As a consequence energy is released when such an amino acid is transferred for example from ethanol to water.

The values for the relative hydrophobicity of the individual amino acids are compiled in the following Table 1.

Table 1

Amino acids	Relative hydrophobicity (kcal/mol)
Gl	0
Leu	1.8
Ile	2.5
Val	1.5
Ala	0.5
Phe	2.5
Cys	- 2.8
Met	1.3
Thr	0.4
Ser	- 0.3
Trp	3.4
Tyr	2.3
Gln	- 0.3
Lys	- 4.2
Asn	- 0.2
Glu	- 9.9
His	0.5
Asp	- 7.4
Arg	- 11.2
Pro	- 3.3

It is apparent from this table that the amino acids cysteine, proline and in particular glutamate, aspartate, arginine and lysine have a high negative relative hydrophobicity.

It was surprisingly found that the activation of recombinant proteins is considerably improved by adding helper sequences 2 to 50 amino acids in length to a protein sequence if these helper sequences have a total relative hydrophobicity which is negative. The length of these helper sequences is preferably 2 to 20, particularly preferably 5 to 20 amino acids.

In addition it is preferred that the quotients for these helper sequences of relative hydrophobicity to the number of amino acids is - 2.0 kcal/mol or less, particularly preferably - 2.5 kcal/mol or less and most preferably - 2.8 kcal/mol or less.

The addition of helper sequences to the recombinant protein can be carried out by means of the usual techniques in the area of molecular biology. This is preferably carried out by adding an oligonucleotide sequence to one or both ends of the DNA sequence coding for a recombinant protein to be expressed, which oligonucleotide codes for one of the protein helper sequences described above with a negative relative hydrophobicity. For this purpose DNA fragments which contain a region which codes for the beginning or for the end of the corresponding gene are for example isolated from the gene to be expressed. Synthetic oligonucleotides which contain regions coding for the helper sequences can then be inserted into these DNA fragments e.g. by using other restriction cleavage sites. Another possibility is to completely replace the natural DNA fragments from the gene by oligonucleotide sequences. Modified DNA sequences can be obtained in this way which contain the information for the added helper sequences in addition to the information for a recombinant protein.

It is expedient to use DNA sequences whose codon usage is adapted to the expression organism (E.L. Winnacker, Gene und Klone, Verlag Chemie, 1985, 224-241) as DNA sequences which code for the N-terminal helper sequences.

In this case when E. coli is the expression organism the following codons are preferred for the following amino acids:

threonine	ACA
proline	CCA
leucine	CTA
lysine	AAA
alanine	GCC
glutamic acid	GAA

A DNA modified in this way which codes for a recombinant protein with added helper sequences is introduced by transformation into a host cell, preferably into a prokaryotic cell, particularly preferably into an E. coli cell. Subsequently the transformed cells are cultured in a suitable medium, the cells are lysed and the recombinant protein which forms in an at least partially inactive state and in particular is present in the form of inclusion bodies, is isolated. Subsequently this protein is solubilized and renatured, preferably at a pH at which the protein can take up its native conformation. These steps in the procedure can be carried out according to techniques which are already known such as for example those which are quoted in the state of the art referred to in the introduction to the description. The activation of the protein is preferably carried out by means of a pulse renaturation such as that disclosed for example in EP-A 0 241 022. The improvement of the known procedures achieved by the

present invention is based in particular on the presence of helper sequences which are added to the N- or/and C-terminus of the recombinant protein. In these procedures the helper sequences are preferably added to the N-terminus of the protein to be activated. However, the attachment of helper sequences to the C-terminus also produces positive results.

Preferred helper sequences are those which contain at least 2 amino acids selected from the group comprising glutamate, aspartate, lysine, arginine and proline, whereby lysine and glutamate residues are particularly preferred and glutamate residues are the most preferred. In addition it is particularly preferred that the helper sequences contain two of the afore-mentioned charged amino acids (i.e. glutamate, aspartate, lysine and arginine) in succession each having the same charge, preferably two successive lysine or glutamate residues, especially preferably two successive glutamate residues.

If the recombinant proteins produced by the process according to the present invention are later to be used therapeutically, it is advantageous that they have a cleavage site at the junction between the helper sequences and the desired protein. By this means the protein can be obtained with its natural amino acid sequence. This cleavage site can be a sequence which is recognized by a protease or by a chemical cleavage reagent for proteins (e.g. BrCN), whereby a protease cleavage site is preferred. It is particularly preferred that the cleavage site is an IgA protease cleavage site such as that described in WO 91/11520. The exact cleavage conditions are also specified in WO 91/11520. In addition a cleavage site which is a cleavage site for factor Xa is also preferred.

Such a cleavage site in the protein sequence is not necessary when using the recombinant protein for analytical purposes.

Concrete examples of helper sequences which are suitable for improving protein activation are the following sequences added to the N-terminus of a protein:

Met-Glu (SEQ ID NO: 1)
Met-Thr-Pro-Leu-Pro-Arg-Pro-Pro (SEQ ID NO: 2)
Met-Thr-Pro-Leu-His-His-Pro-Arg-Pro-Pro
(SEQ ID NO: 3)
Met-Thr-Pro-Leu-Lys-Lys-Pro-Arg-Pro-Pro
(SEQ ID NO: 4)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Pro-Arg-Pro-Pro
(SEQ ID NO: 5)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Thr-Pro-Leu-Pro-Arg-Pro-Pro (SEQ ID NO: 6)
Met-Thr-Pro-Leu-Glu-Glu-Gln-Pro-Pro (SEQ ID NO: 7)
Met-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro
(SEQ ID NO: 8)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Ile-Glu-Gly-Arg
(SEQ ID NO: 9)
Met-Thr-Pro-Leu-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro (SEQ ID NO: 10)

The helper sequences SEQ ID NO: 5, 6, 7 and 9 which have two successive glutamate residues result in the highest renaturation yields and are therefore the most preferred.

The process according to the present invention is especially suitable for the activation of recombinant human proteins and their derivatives produced in prokaryotes, such as e.g. plasminogen activators, interferons, interleukins and granulocyte colony

stimulating factors. It is particularly preferred that the protein to be activated is a granulocyte colony stimulating factor (G-CSF) which has the initial DNA sequence ACACCA. Derivatives of G-CSF which are disclosed in EP-A 0 456 200 are also preferred.

The vector pKK177-3-G-CSF Bg was deposited under the number DSM 5867 at the Deutsche Sammlung Für Mikroorganismen, Grisebachstr. 8, D-3400 Göttingen on 28 March, 1990.

It is intended to elucidate the invention further by the following examples and figures.

Figure 1 shows the dependence of the renaturation yield on the concentration (arginine concentration 0.2 mol/l) for constructs which contain sequences corresponding to sequence 0 of table 2 (curve 1), SEQ ID NO:3 (curve 2), SEQ ID NO:5 (curve 3) and SEQ ID NO:8 (curve 4).

Figure 2 shows the dependence of the renaturation yield on the concentration (arginine concentration 0.8 mol/l) for constructs which contain sequences corresponding to sequence 0 of table 2 (curve 1), SEQ ID NO:3 (curve 2), SEQ ID NO:5 (curve 3) and SEQ ID NO:8 (curve 4).

Figure 3 shows the dependence of the renaturation yield on the arginine concentration (curve nomenclature is analogous to Figure 1 and 2).

Figure 4 shows the reactivation yield in relation to the incubation time (arginine concentration 0.2 mol/l, curve nomenclature is analogous to Figure 1 and 2).

Example 1

Construction of the vectors

The vector pKK177-3 G-CSF Bg (DSM 5367) is digested with EcoRI (partially) and ApaI and the oligonucleotide

EcoRI

ApaI

AATTCGGAGGAAAAATTA | ATG ..... | ACACCACTGGGCC

| Met..... | G-CSF sequence without ATG

is inserted into the linearized vector fragment (ca. 3450 bp) which formed.

AATTCGGAGGAAAAATTA: SEQ ID NO: 11

ACACCACTGGGCC: SEQ ID NO: 12

Each of the DNA sequences used in the gap conforms with the genetic code for the amino acids listed in Table 2, i.e. an oligonucleotide with the genetic code for Met-Thr-Pro-Leu-Pro-Arg-Pro-Pro (SEQ ID NO: 2) for construct (2). The plasmids resulting for ligation of the oligonucleotides into the cleaved vector are transformed into E. coli HB101. In order to ensure a better regulation of the tac promoter, the cells were additionally transformed with a plasmid compatible with pBP010 (preparation cf. European Patent application No. 91 111 155.7) which contains the $lacI^q$ gene. The $lacI^q$ gene has been known for a long time to one skilled in the art and is easily obtainable. Examples of suitable plasmids which are compatible with pBP010 are e.g. pACYC 177 (DSM 3693P) into which the $lacI^q$ gene is inserted or plasmids derived therefrom

(cf. e.g. Gene 85 (1989), 109-114 and EP-A 0 373 365). The resulting clones are selected on kanamycin (50 µg/ml)/ampicillin (50 µg/ml) and identified by means of restriction analysis. When cleaved with EcoRI and EcoRV fragments result with lengths of ca. 3.15 kb, ca. 0.3 kb (with the respective constructs) and 4.85 kb.

Example 2

a) Fermentation:

Clones which were identified as positive according to Example 1 are grown in 5 ml culture in LB medium containing kanamycin and ampicillin (for concentrations see Example 1) up to an OD_{550} of 0.5, induced with 5 mmol/l IPTG and incubated for 3 hours at 37°C. 10 OD of this induced culture is harvested and a total cell extract is prepared from this. The total cell extract is analyzed on a SDS page gel.

When it is apparent from this that the desired protein is being expressed, the culture is repeated on a 1 l scale, the cells are harvested and an IB preparation is carried out.

b) IB preparation:

The cells are harvested by centrifugation, taken up in 100 ml Tris magnesium buffer (10 mmol/l Tris, pH 8.0, 1 mmol/l $MgCl_2$) and lysed with lysozyme (0.3 mg/ml).

They are incubated for 15 minutes at 37°C and subjected to one passage of a French press (1200 psi).

Subsequently a DNAse digestion (2 mg DNAse I) is carried out for 30 minutes at 37°C.

20 ml 0.5 mol/l NaCl, 20 mmol/l EDTA, pH 8.0 and 3 ml 20 % Triton X 100 is added and incubated for 10 minutes at room temperature.

The suspension is centrifuged for 10 minutes at 15000 rpm at 4°C. The pellet is taken up in 30 ml 50 mmol/l Tris, pH 8.0, 50 mmol/l EDTA and 0.5 % Triton X 100 and treated with ultrasound. It is centrifuged again, resuspended and treated with ultrasound. This procedure is repeated twice again. Subsequently it is centrifuged and the pellets obtained in this way are used as IBs in Example 3.

Example 3

Solubilization/renaturation

a) Solubilization

Solubilization buffer:
6 mol/l guanidine hydrochloride
0.1 mol/l Tris buffer, pH 8.0
1 mmol/l EDTA
100 mmol/l DTE (dithioerythreitiol)

Dialysis buffer 1:
6 mol/l guanidine hydrochloride
3 mmol/l EDTA at pH 3.0

1 g inclusion bodies is added to 30 ml solubilization buffer, homogenized for 5 minutes with ultrasound and incubated for 1 hour at room temperature. HCl is added until the pH reaches 3.0. Insoluble material is subsequently removed by centrifugation.

It is dialyzed against dialysis buffer 1 until the DTE is completely removed (≤ 1 mmol/l DTE).

b) Pulse reactivation:

Renaturation buffer:
0.8 mol/l arginine hydrochloride
0.1 mol/l Tris buffer, pH 8.0
0.5 mmol/l GSH
0.5 mmol/l GSSG
1 mmol/l EDTA

Dialysis buffer 2:
10 mmol/l Tris buffer, pH 8.0
1 mmol/l EDTA

The pulse reactivation is carried out as described in EP-A 0 241 022. A device according to Fig. 5 of EP-A 0 241 022 is used.

For this protein is added to the reaction volume (100 ml renaturation buffer) at intervals of 30 minutes so that the protein concentration in the reaction volume increases by 50 µg/ml per pulse. Altogether it is pulsed 20 times (final concentration ca. 1 mg/ml reaction volume).

After the pulse reactivation turbidities are removed from the reaction volume by centrifugation and the total reaction volume is dialyzed against dialysis buffer 2 until arginine has been removed (≤ 50 mmol/l). (It is expedient to check this by measuring the conductivity. The dialysis can be finished when the conductivities of dialysis buffer and reaction volume are identical.) The reactivation yields for the individual constructs which were determined by means of an activity test are shown in Table 2.

Table 2

	% Renaturation[2]	Relative hydrophobicity (kcal/mol)	rel. hydrophobicity: number of amino acids
(0) Met-G-CSF[1]	10	1,3	1,3
(1) Met-Glu-G-CSF	50	- 6,6	- 4,3
(2) Met-Thr-Pro-Leu-Pro-Arg-Pro-Pro-G-CSF	20	- 20,9	- 2,6
(3) Met-Thr-Pro-Leu-His-His-Pro-Arg-Pro-Pro-G-CSF	20	- 19,9	- 2
(4) Met-Thr-Pro-Leu-Lys-Lys-Pro-Arg-Pro-Pro-G-CSF	50	- 29,3	- 2,9
(5) Met-Thr-Pro-Leu-Glu-Glu-Gly-Pro-Arg-Pro-Pro-G-CSF	80-90	- 40,7	- 3,7
(6) Met-Thr-Pro-Leu-Glu-Glu-Gly-Thr-Pro-Leu-Pro-Arg-Pro-Pro-G-CSF	80	- 41,8	- 2,9
(7) Met-Thr-Pro-Leu-Glu-Glu-Gln-Pro-Pro-G-CSF	80	- 26,5	- 2,9
(8) Met-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro-G-CSF	60	- 44,3	- 3,4
(9) Met-Thr-Pro-Leu-Glu-Glu-Gly-Ile-Glu-Gly-Arg-G-CSF	80	- 38,1	- 3,5
(10) Met-Thr-Pro-Leu-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro-G-CSF	50	- 45,4	- 2,8

[1] not an example according to the present invention

[2] determined with the G-CSF activity test according to Example 3

(1) to (10) : SEQ ID NO: 1 to 10 bound to the G-CSF sequence without an N-terminal methionine residue

Example 4

Determination of the G-CSF activity

The activity of G-CSF is tested as described Biochem.J. 253 (1988) 213-218, Exp. Hematol. 17 (1989) 116-119, Proc.Natl.Acad.Sci. USA 83 (1986) 5010, using the murine leukemia line NFS60 which is completely dependent on G-CSF. The medium (RPMI medium, Boehringer Mannheim GmbH, Order No. 2099445 with 10 % foetal calf serum) of the maintenance culture permanently contains 1000 U/ml G-CSF to preserve the factor dependency of the cells.

This test directly measures the G-CSF-stimulated proliferation of NFS60 cells by means of the incorporation of ^{3}H-thymidine. The test is carried out in the following manner:

NFS60 cells which are in the exponential growth phase (cell density is at most $1x10^{5}$ cells/ml) are transferred to microtitre plates ($1x10^{4}$ cells/well) and cultured with a decreasing G-CSF concentration. The maximum dose of G-CSF in well 1 corresponds to the concentration in the maintenance culture (1000 U/ml, specific activity $1x10^{8}$ U/mg protein). The dilution steps are by factors of ten.

After an incubation of about 24 hours, ^{3}H-thymidine (0.1 µCi/well) is added. After this the cells are incubated for a further 16 hours.

In order to evaluate the test the cells are frozen in the microtitre plate in order to lyse them. The cell lysate is aspirated on a glass fibre filter, rinsed,

dried and measured in a scintillation counter. The incorporation of ^{3}H-thymidine is proportional to the G-CSF-induced proliferation of the NFS60 cells.

Example 5

Determination of the dependence of renaturation yield on the concentration of denatured protein after a single addition.

Starting material: inclusion bodies having the constructs No. 0/3/5 and 8 of Table 2.

Solubilization and first dialysis:

The IB material is solubilized according to Example 3, dialyzed to remove the reducing agent and subsequently adjusted to a protein concentration of 30 mg/ml (M.M. Bradford, Anal.Biochem. 72 (1976) 255).

Renaturation:

The reactivation is carried out in 0.8 mol/l or 0.2 mol/l arginine hydrochloride, 10 mmol/l EDTA, 0.5 mmol/l GSH and 0.5 mmol/l GSSG at 20°C and pH 8.0.

The protein concentrations in the respective renaturation preparations were adjusted to between 0.3 and 3 mg/ml. The concentration of guanidine hydrochloride was 0.55 mol/l in all the preparations.

After an incubation of 3 hours at room temperature the reaction was stopped by acidification (pH 4.5).

The ratio of denatured to renatured protein was determined by HPLC.

Mobile buffer A: 0.12 % (v/v) trifluoroacetic acid
Mobile buffer B: 90 % (v/v) acetonitrile , 0.1 % (v/v) trifluoroacetic acid
Gradient of B: 40 to 70 % in 30 min
Flow rate: 1 ml/min, detection at 280 nm

The results are shown in Figure 1 and 2.

Example 6

Dependence of the renaturation on the arginine concentration

Dialyzed solubilizates (protein concentration 10 mg/ml) of the constructions 0,3,5 and 8 (Tab. 2) which were prepared analogous to Example 5 served as the starting material.

The protein concentration in the renaturation buffer (0 to 0.8 mol/l arginine hydrochloride, 100 mmol/l Tris, 10 mmol/l EDTA, 0.5 mmol/l GSH, 0.5 mmol/l GSSG, room temperature at pH 8) was adjusted to 1 mg/ml by a single addition of denatured protein.

After an incubation period of 3 h the reaction was stopped by acidification (pH 4.5). The subsequent evaluation was carried out by HPLC analogous to Example 5.

The results are shown in Figure 3.

Example 7

Kinetics of the reactivation in 0.2 mol/l arginine buffer

Starting material: the solubilisates of Example 6 were used.

The reactivation was carried out in 0.2 mol/l arginine hydrochloride, 100 mmol/l Tris, 10 mmol/l EDTA, 0.5 mmol/l GSH, 0.5 mmol/l GSSG, at room temperature and pH 8. The protein concentration in the reaction preparation was adjusted by a single addition to 1 mg/ml and the guanidine concentration was adjusted to 0.55 mol/l. Samples were taken at 5, 10, 15, 60 and 180 minutes, the reaction was stopped in each case by acidification (pH 4.5) and subsequently the reactivation kinetics were determined by HPLC (cf. Example 5).

Figure 4 shows the dependence of the reactivation yield on the incubation period.

SEQUENCE LISTING

(iii) NUMBER OF SEQUENCES: 12

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu
1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Pro Leu Pro Arg Pro Pro
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Pro Leu His His Pro Arg Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Pro Leu Lys Lys Pro Arg Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Thr Pro Leu Glu Glu Gly Pro Arg Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Pro Leu Glu Glu Gly Thr Pro Leu Pro Arg Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Thr Pro Leu Glu Glu Gln Pro Pro
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Ala Lys Arg Phe Lys Lys His Pro Arg Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Pro Leu Glu Glu Gly Ile Glu Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Pro Leu Lys Ala Lys Arg Phe Lys Lys His Pro Arg Pro Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGGAGG AAAAATTA 18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACACCACTGG GCC 13

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. Process for the activation of recombinant proteins which are present in at least a partially inactive form, wherein a protein is activated by known solubilisation or/and renaturation techniques, said protein having additional helper sequences 2 to 50 amino acids in length at its N- or/and C-terminus added to said recombinant protein by adding oligonucleotide sequence encoding said helper sequence to at least one end of a DNA sequence encoding said recombinant protein and whereby the relative hydrophobicity of these helper sequences, which is calculated as the sum of the relative hydrophobicities specified in Table 1 for the individual amino acids, has a negative numerical value.

2. Process as claimed in claim 1, w h e r e i n the helper sequences have a value for the ratio of relative hydrophobicity to the number of amino acids which is -2.0 kcal/mol or less.

3. Process as claimed in claim 2, w h e r e i n the helper sequences have a value for the ratio of relative hydrophobicity to the number of amino acids which is -2.5 kcal/mol or less.

4. Process as claimed in one of the previous claims, w h e r e i n the helper sequences are added to the N-terminus of the protein to be activated.

5. Process as claimed in one of the claims 1 to 3, w h e r e i n the helper sequences are added to the C-terminus of the protein to be activated.

6. Process as claimed in one of the previous claims, w h e r e i n the helper sequences contain at least two amino acids selected from the group comprising glutamate, aspartate, lysine, arginine and proline.

7. Process as claimed in claim 6, w h e r e i n the helper sequences contain at least two glutamate residues.

8. Process as claimed in claim 6 or 7, w h e r e i n the helper sequences contain two successive amino acids having the same charge selected from the group comprising glutamate, aspartate, lysine and arginine.

9. Process as claimed in claim 8, w h e r e i n the helper sequences contain two successive glutamate residues.

10. Process as claimed in one of the previous claims, w h e r e i n proteins are activated which have a cleavage site at the junction between the helper sequences and the desired protein.

11. Process as claimed in claim 10, w h e r e i n the cleavage site is a sequence recognized by a protease.

12. Process as claimed in claim 11, w h e r e i n the cleavage site is an IgA protease cleavage site.

13. Process as claimed in claim 12, w h e r e i n the cleavage site is a factor Xa cleavage site.

14. Process as claimed in one of the previous claims, w h e r e i n a protein is activated which contains a N-terminal helper sequence having one of the sequences specified in the following:
Met-Glu (SEQ ID NO:1)
Met-Thr-Pro-Leu-Pro-Arg-Pro-Pro (SEQ ID NO: 2)
Met-Thr-Pro-Leu-His-His-Pro-Arg-Pro-Pro
(SEQ ID NO: 3)
Met-Thr-Pro-Leu-Lys-Lys-Pro-Arg-Pro-Pro
(SEQ ID NO: 4)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Pro-Arg-Pro-Pro
(SEQ ID NO: 5)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Thr-Pro-Leu-Pro-Arg-Pro-Pro (SEQ ID NO: 6)
Met-Thr-Pro-Leu-Glu-Glu-Gln-Pro-Pro (SEQ ID NO: 7)
Met-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro
(SEQ ID NO: 8)
Met-Thr-Pro-Leu-Glu-Glu-Gly-Ile-Glu-Gly-Arg
(SEQ ID NO: 9)
Met-Thr-Pro-Leu-Lys-Ala-Lys-Arg-Phe-Lys-Lys-His-Pro-Arg-Pro-Pro (SEQ ID NO: 10)

15. Process as claimed in one of the previous claims, w h e r e i n a protein is activated said protein being granulocyte colony stimulating factor (G-CSF) or derivatives thereof.

16. A process as claimed in claim 1, substantially as hereinbefore described with reference to the drawings and/or Examples.

~~17. The steps, features, compositions and compounds~~ disclosed herein or referred to or indicated in the specification and/or claims of this application, individually or collectively, and any and all combinations ~~of any two or more of said steps or features.~~

DATED this FOURTEENTH day of FEBRUARY 1992

Boehringer Mannheim GmbH

by DAVIES COLLISON CAVE
Patent Attorneys for the applicant(s)

Abstract

A process for the activation of recombinant proteins which are present in at least a partially inactive form in which a protein is activated by known solubilization or/and renaturation techniques, said protein having additional helper sequences 2 to 50 amino acids in length at its N- or/and C-terminus whereby the relative hydrophobicity of these helper sequences which is calculated as the sum of the relative hydrophobicity specified in Table 1 for the individual amino acids has a negative numerical value.

Fig.1

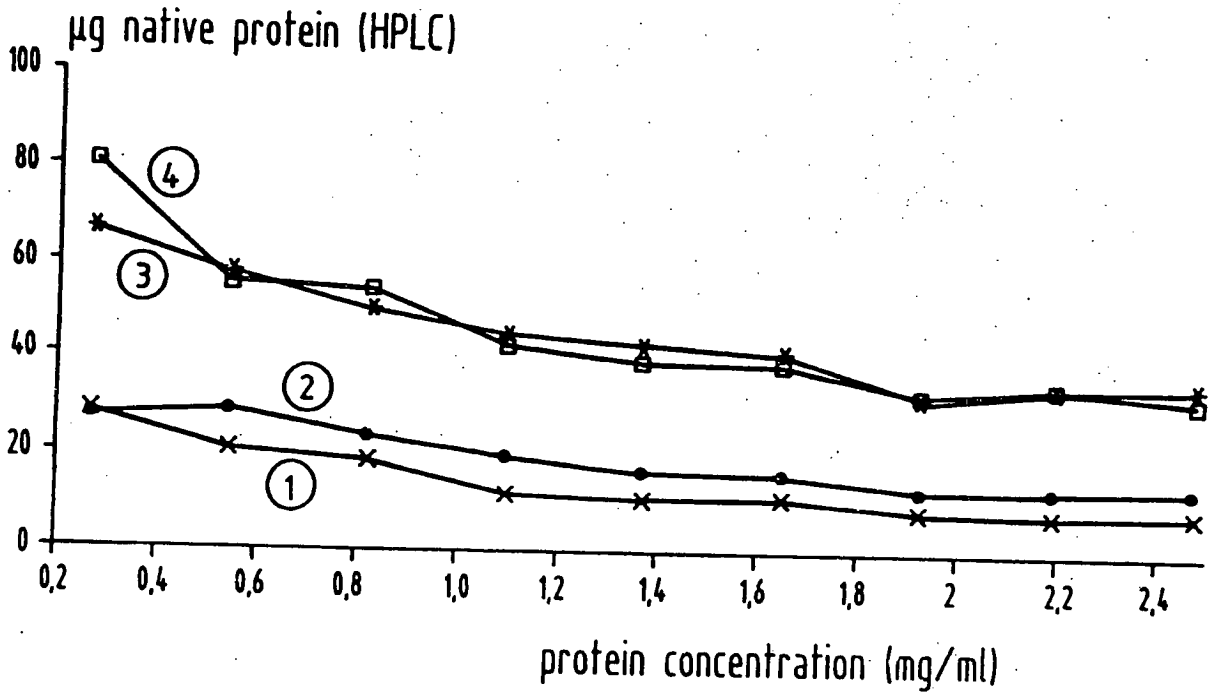

µg native protein (HPLC)
100
80
60
40
20
0
0,2
0,4
0,6
0,8
1,0
1,2
1,4
1,6
1,8
2
2,2
2,4
4
3
2
1
protein concentration (mg/ml)

Fig.2

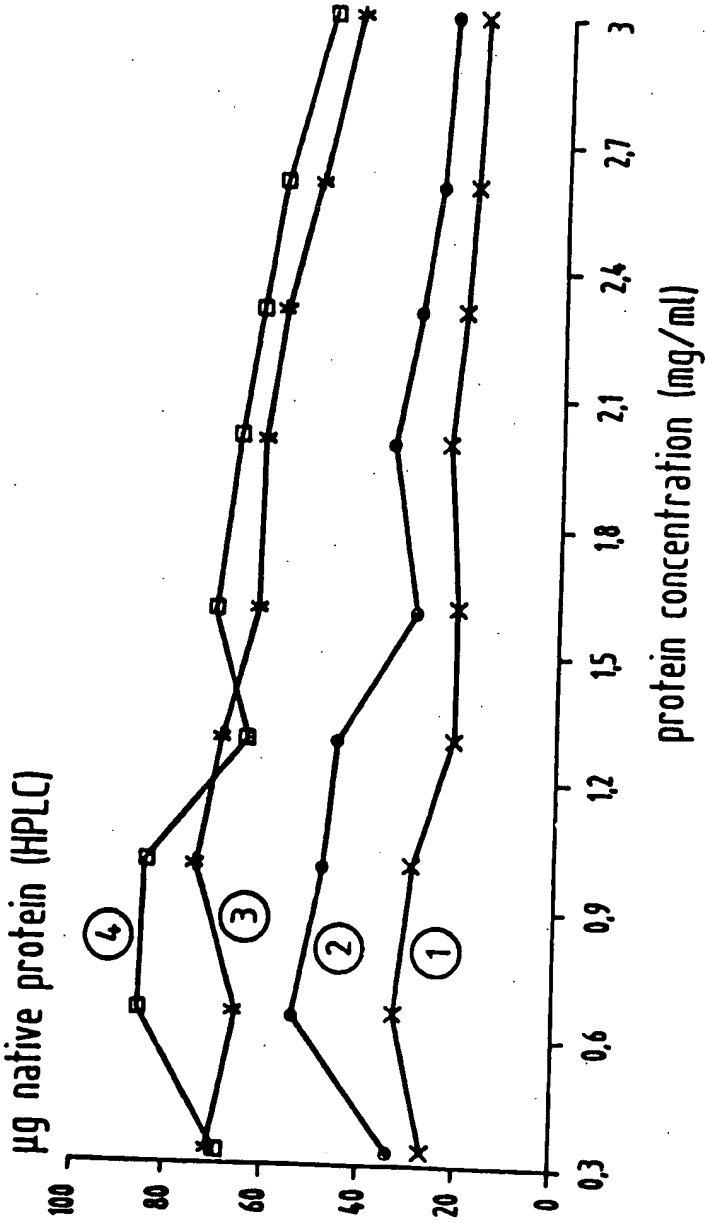

µg native protein (HPLC)
100
80
60
40
20
0
0,3
0,6
0,9
1,2
1,5
1,8
2,1
2,4
2,7
3
protein concentration (mg/ml)
1
2
3
4

Fig.3

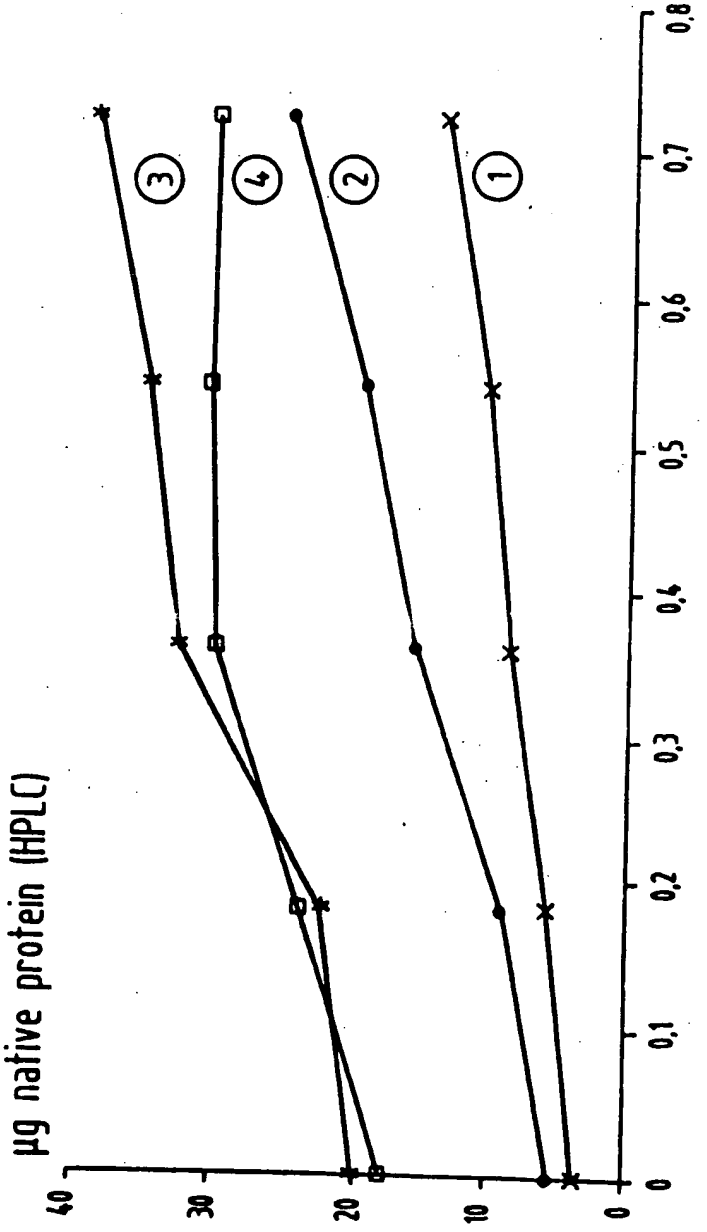
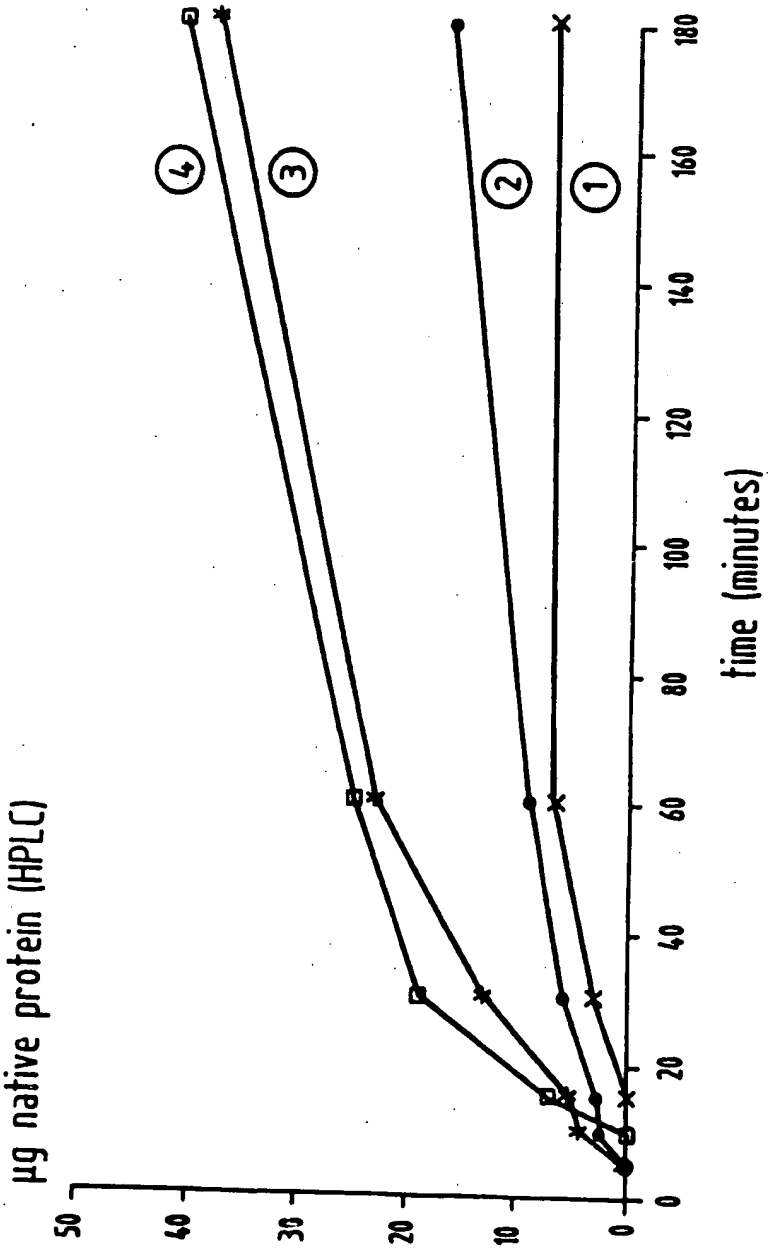

µg native protein (HPLC)
40
30
20
10
0
0
0,1
0,2
0,3
0,4
0,5
0,6
0,7
0,8
arginine (mol/l)
1
2
3
4

Fig. 4


µg native protein (HPLC)
50
40
30
20
10
0
0
20
40
60
80
100
120
140
160
180
time (minutes)
1
2
3
4